SEQUENCE LISTING

<110> The Scripps Research Institute
The Regents of the University of California
Wu, Eugene
Nemerow, Glen R.
Stewart, Phoebe

<120> MODIFIED FIBER PROTEINS FOR EFFICIENT RECEPTOR BINDING

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<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
tgtacaccgg atccggcgca cacc 24

<210> 26
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 26
cacaacgagc tcaattaatt aattgccaca tcctc 35

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27

cgcgctgact cttaaggact agtttc 26

<210> 28
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28
gcgcttaatt aacatcatca taatatacc ttatttt 37

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
atcatggccg acaagcagaa gaac 24

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
gtacagctcg tccatgccga gagt 24

<210> 31
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFP probe

<221> misc_feature
<222> 1
<223> FAM (6-carboxy-fluorescein)

<221> misc_feature
<222> 26
<223> TAMRA (6-carboxy-tetramethyl-rhodamine)

<400> 31
caggaccatg tgatcgcgct tctcgt 26

<210> 32
<211> 1749
<212> DNA
<213> Adenovirus serotype 2 fiber

<220>
<221> CDS

<222> (1)...(1749)

<400> 32

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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15

tat gac aca gaa acc ggg cct cca act gtg ccc ttt ctt acc cct cca   96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30

ttt gtt tca ccc aat ggt ttc caa gaa agt ccc cct gga gtt ctc tct  144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45

cta cgc gtc tcc gaa cct ttg gac acc tcc cac ggc atg ctt gcg ctt  192
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60

aaa atg ggc agc ggt ctt acc cta gac aag gcc gga aac ctc acc tcc  240
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
65                  70                  75                  80

caa aat gta acc act gtt act cag cca ctt aaa aaa aca aag tca aac  288
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95

ata agt ttg gac acc tcc gca cca ctt aca att acc tca ggc gcc cta  336
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
            100                 105                 110

aca gtg gca acc acc gct cct ctg ata gtt act agc ggc gct ctt agc  384
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
        115                 120                 125

gta cag tca caa gcc cca ctg acc gtg caa gac tcc aaa cta agc att  432
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
    130                 135                 140

gct act aaa ggg ccc att aca gtg tca gat gga aag cta gcc ctg caa  480
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

aca tca gcc ccc ctc tct ggc agt gac agc gac acc ctt act gta act  528
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
                165                 170                 175

gca tca ccc ccg cta act act gcc acg ggt agc ttg ggc att aac atg  576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
            180                 185                 190

gaa gat cct att tat gta aat aat gga aaa ata gga att aaa ata agc  624
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser
        195                 200                 205

ggt cct ttg caa gta gca caa aac tcc gat aca cta aca gta gtt act  672
Gly Pro Leu Gln Val Ala Gln Asn Ser Asp Thr Leu Thr Val Val Thr
    210                 215                 220

gga cca ggt gtc acc gtt gaa caa aac tcc ctt aga acc aaa gtt gca  720
Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala
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225                 230                 235                 240

gga gct att ggt tat gat tca tca aac aac atg gaa att aaa acg ggc   768
Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly
                245                 250                 255

ggt ggc atg cgt ata aat aac aac ttg tta att cta gat gtg gat tac   816
Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr
            260                 265                 270

cca ttt gat gct caa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc   864
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro
        275                 280                 285

ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc   912
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly
    290                 295                 300

cta tac ctt ttt aat gca tca aac aat act aaa aaa ctg gaa gtt agc   960
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser
305                 310                 315                 320

ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata  1008
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile
                325                 330                 335

aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca  1056
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro
            340                 345                 350

gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat  1104
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn
        355                 360                 365

gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac  1152
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp
    370                 375                 380

aac tca ggg gcc att aca ata gga aac aaa aat gat gac aaa ctt acc  1200
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr
385                 390                 395                 400

ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat  1248
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp
                405                 410                 415

aat gac tgc aaa ttt act ttg gtt ctt aca aaa tgt ggg agt caa gta  1296
Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val
            420                 425                 430

cta gct act gta gct gct ttg gct gta tct gga gat ctt tca tcc atg  1344
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met
        435                 440                 445

aca ggc acc gtt gca agt gtt agt ata ttc ctt aga ttt gac caa aac  1392
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn
    450                 455                 460

ggt gtt cta atg gag aac tcc tca ctt aaa aaa cat tac tgg aac ttt  1440
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe
465                 470                 475                 480
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aga aat ggg aac tca act aat gca aat cca tac aca aat gca gtt gga   1488
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly
                485                 490                 495

ttt atg cct aac ctt cta gcc tat cca aaa acc caa agt caa act gct   1536
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala
            500                 505                 510

aaa aat aac att gtc agt caa gtt tac ttg cat ggt gat aaa act aaa   1584
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys
        515                 520                 525

cct atg ata ctt acc att aca ctt aat ggc act agt gaa tcc aca gaa   1632
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu
    530                 535                 540

act agc gag gta agc act tac tct atg tct ttt aca tgg tcc tgg gaa   1680
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu
545                 550                 555                 560

agt gga aaa tac acc act gaa act ttt gct acc aac tct tac acc ttc   1728
Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe
                565                 570                 575

tcc tac att gcc cag gaa taa                                     1749
Ser Tyr Ile Ala Gln Glu  *
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<210> 33
<211> 582
<212> PRT
<213> Adenovirus serotype 2 fiber

<400> 33

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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
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Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
            100                 105                 110
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
        115                 120                 125
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
    130                 135                 140
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
145                 150                 155                 160
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
                165                 170                 175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
            180                 185                 190
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser
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Gly Pro Leu Gln Val Ala Gln Asn Ser Asp Thr Leu Thr Val Val Thr
195 200 205
Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala
210 215 220
Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly
225 230 235 240
Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr
245 250 255
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro
260 265 270
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly
275 280 285
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser
290 295 300
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile
305 310 315 320
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro
325 330 335
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn
340 345 350
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp
355 360 365
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr
370 375 380
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp
385 390 395 400
Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val
405 410 415
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met
420 425 430
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn
435 440 445
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe
450 455 460
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly
465 470 475 480
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala
485 490 495
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys
500 505 510
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu
515 520 525
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu
530 535 540
Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe
545 550 555 560
Ser Tyr Ile Ala Gln Glu
565 570 575
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<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber

<220>
<221> CDS
<222> (1)...(1746)

<400> 34

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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc   96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc  240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac  288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta  336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc  384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att  432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa  480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act  528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                 170                 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg  576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg  624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act  672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                 215                 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act  720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca  768
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Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt   816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                 265                 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275                 280                 285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290                 295                 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata  1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                 330                 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca  1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340                 345                 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat  1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac  1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370                 375                 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act  1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390                 395                 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag  1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                 410                 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata  1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420                 425                 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata  1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435                 440                 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat  1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450                 455                 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt  1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465                 470                 475                 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga  1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
```

```
                485                 490                 495
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500                 505                 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515                 520                 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530                 535                 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                 550                 555                 560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca   1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565                 570                 575

tac att gcc caa gaa taa                                          1746
Tyr Ile Ala Gln Glu  *
            580
```

<210> 35
<211> 581
<212> PRT
<213> Adenovirus serotype 5 fiber

<400> 35

```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                 170                 175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                 215                 220
```

```
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                 265                 270
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290                 295                 300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                 330                 335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340                 345                 350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370                 375                 380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390                 395                 400
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                405                 410                 415
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420                 425                 430
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435                 440                 445
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450                 455                 460
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465                 470                 475                 480
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
                485                 490                 495
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500                 505                 510
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
        515                 520                 525
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530                 535                 540
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                 550                 555                 560
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565                 570                 575
Tyr Ile Ala Gln Glu
            580
```

<210> 36
<211> 1098
<212> DNA
<213> Adenovirus serotype 37 fiber

<220>
<221> CDS
<222> (1)...(1098)

<400> 36

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atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc   48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
```

```
tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt    96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
                20                  25                  30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc   144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
            35                  40                  45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag   192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
        50                  55                  60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct   240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80

aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat   288
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85                  90                  95

gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga   336
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
            100                 105                 110

cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat   384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115                 120                 125

tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa   432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130                 135                 140

aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta   480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                 150                 155                 160

aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca   528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                165                 170                 175

tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca   576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
            180                 185                 190

tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg   624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
        195                 200                 205

gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att   672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                 215                 220

gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa   720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
225                 230                 235                 240

ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt   768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
                245                 250                 255
```

```
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga   816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
            260                 265                 270

aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct   864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
        275                 280                 285

aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga   912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290                 295                 300

gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca   960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                 310                 315                 320

gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct  1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
                325                 330                 335

atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt  1056
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340                 345                 350

gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga          1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  *
        355                 360                 365
```

<210> 37
<211> 365
<212> PRT
<213> Adenovirus serotype 37 fiber

<400> 37

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Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50                  55                  60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85                  90                  95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
            100                 105                 110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115                 120                 125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130                 135                 140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                 150                 155                 160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                165                 170                 175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
            180                 185                 190
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
```

```
        195                 200                 205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                 215                 220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
225                 230                 235                 240
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
                245                 250                 255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
            260                 265                 270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
        275                 280                 285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290                 295                 300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                 310                 315                 320
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
                325                 330                 335
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340                 345                 350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        355                 360                 365
```

<210> 38
<211> 1098
<212> DNA
<213> Adenovirus serotype 19p fiber

<220>
<221> CDS
<222> (1)...(1098)

<400> 38

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atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc   48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                  10                  15

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt   96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc   144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag   192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50                  55                  60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct   240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80

aag gct cca ctg caa gtt act act gat aaa aaa ctt gag ctt gca tat   288
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85                  90                  95

gat aat cca ttt gaa tgt agt gct aat aaa ttt agt tta aaa gta gga   336
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
            100                 105                 110
```

```
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat   384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115                 120                 125

tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa   432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130                 135                 140

aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta   480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                 150                 155                 160

aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca   528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                165                 170                 175

tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca   576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
            180                 185                 190

tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg   624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
        195                 200                 205

gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att   672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                 215                 220

gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa   720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
225                 230                 235                 240

ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt   768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
                245                 250                 255

tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga   816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
            260                 265                 270

aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct   864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
        275                 280                 285

aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga   912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290                 295                 300

gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca   960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                 310                 315                 320

gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct  1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
                325                 330                 335

atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt  1056
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340                 345                 350

gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga          1098
```

Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *
355 360 365

<210> 39
<211> 365
<212> PRT
<213> Adenovirus serotype 19p fiber

<400> 39
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1 5 10 15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
20 25 30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
35 40 45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
50 55 60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65 70 75 80
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
85 90 95
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
100 105 110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
115 120 125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
130 135 140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145 150 155 160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
165 170 175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
180 185 190
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
195 200 205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
210 215 220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
225 230 235 240
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
245 250 255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
260 265 270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
275 280 285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
290 295 300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305 310 315 320
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
325 330 335
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
340 345 350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
355 360 365

<210> 40
<211> 1228

<212> DNA
<213> Adenovirus serotype 9 fiber

<220>
<221> CDS
<222> (50)...(1138)

<400> 40
aagggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag 58
Met Ser Lys
1

agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat ggc tac 106
Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr
5 10 15

gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc 154
Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
20 25 30 35

gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct 202
Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
40 45 50

gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg 250
Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly
55 60 65

ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat 298
Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp
70 75 80

cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct 346
Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala
85 90 95

cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc 394
Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly
100 105 110 115

ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat 442
Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn
120 125 130

act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat 490
Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp
135 140 145

aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca 538
Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Gly Leu Ser
150 155 160

ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag 586
Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys
165 170 175

cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat 634
Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp
180 185 190 195

cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt 682

```
Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
                200                 205                 210

caa ata ttg gct aat gtg tca tta att gtc gta gat ggt aag tac aaa   730
Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly Lys Tyr Lys
            215                 220                 225

att atc aat aac aat act caa cca gct ctc aaa gga ttt acc att aaa   778
Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe Thr Ile Lys
        230                 235                 240

tta ttg ttt gat gaa aat gga gta ctt atg gaa tct tca aat ctt ggt   826
Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser Asn Leu Gly
    245                 250                 255

aaa tca tat tgg aac ttt aga aat gaa aat tca att atg tca aca gct   874
Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met Ser Thr Ala
260                 265                 270                 275

tat gaa aaa gct att gga ttc atg cct aat ttg gta gcc tat cca aaa   922
Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys
                280                 285                 290

cct acc gct ggc tct aaa aaa tat gca aga gat ata gtt tat gga aac   970
Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Asn
            295                 300                 305

atc tac ctt ggt gga aag cca gat caa cca gta acc att aaa act acc   1018
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile Lys Thr Thr
        310                 315                 320

ttt aat cag gaa act gga tgt gaa tat tct atc aca ttt gat ttt agt   1066
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp Phe Ser
    325                 330                 335

tgg gcc aag act tat gta aat gtt gaa ttt gaa aca acc tct ttt acc   1114
Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
340                 345                 350                 355

ttt tcc tat atc gcc caa gaa tga aagaccaata aacgtgtttt tcatttcaaa  1168
Phe Ser Tyr Ile Ala Gln Glu  *
                360

attttcatgt atctttattg atttttacac cagcacgggt agtcagtctc ccaccaccag 1228
```

<210> 41
<211> 362
<212> PRT
<213> Adenovirus serotype 9 fiber

<400> 41

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Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30
Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45
Lys Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys
    50                  55                  60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val
```

65 70 75 80
Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala
85 90 95
Leu Asp Ala Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala
100 105 110
Gly His Gly Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly
115 120 125
Leu Arg Asn Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
130 135 140
Ser Thr Asp Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly
145 150 155 160
Gly Leu Ser Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys
165 170 175
Glu Asp Lys Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys
180 185 190
Lys Ile Asp Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys
195 200 205
Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly
210 215 220
Lys Tyr Lys Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe
225 230 235 240
Thr Ile Lys Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser
245 250 255
Asn Leu Gly Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met
260 265 270
Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala
275 280 285
Tyr Pro Lys Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val
290 295 300
Tyr Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile
305 310 315 320
Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe
325 330 335
Asp Phe Ser Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr
340 345 350
Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
355 360

<210> 42
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 third repeat

<400> 42
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys
1 5 10 15
Lys Thr Lys Ser
20

<210> 43
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 third repeat

<400> 43
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
1 5 10 15
Lys Thr Lys Ser
20

<210> 44
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat motif

<221> VARIANT
<222> 4
<223> Xaa = Thr or Ser

<400> 44
Thr Thr Val Xaa
1

<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat Consensus Sequence

<221> VARIANT
<222> 3,5,7,13
<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT
<222> 1, 2, 4, 6, 8, 9, 11, 12, 14, 15
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 10
<223> Xaa = Pro or Gly

<400> 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

<210> 46
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 21st repeat

<400> 46
Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
1 5 10 15

<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1 5 10 15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa
1 5

<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5Ds fiber

<221> CDS
<222> (13)...(1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A,T,C or G

<400> 50
atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
30 35 40 45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
50 55 60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
65 70 75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
80 85 90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt 339
Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
95 100 105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt 387
Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
110 115 120 125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat 435
Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
130 135 140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act 483
Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr
145 150 155

ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat 531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn
160 165 170

aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt 579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys
175 180 185

aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa 627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys
190 195 200 205

tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc 675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly
210 215 220

agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata 723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile
225 230 235

```
aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca   771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro
        240                 245                 250

gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat   819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr
    255                 260                 265

aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct   867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser
270                 275                 280                 285

cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac   915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn
                290                 295                 300

gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca   963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr
            305                 310                 315

cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca   1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser
        320                 325                 330

tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc   1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser
    335                 340                 345

tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa 1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu  *
350                 355

gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca         1164

<210> 51
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5deltas

<400> 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys
                85                  90                  95
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr
            100                 105                 110
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn
        115                 120                 125
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu
    130                 135                 140
```

```
Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
145                 150                 155                 160
Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
                165                 170                 175
Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
            180                 185                 190
Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
        195                 200                 205
Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
    210                 215                 220
Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
225                 230                 235                 240
Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
                245                 250                 255
Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
            260                 265                 270
Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
        275                 280                 285
Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys
    290                 295                 300
Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
305                 310                 315                 320
Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
                325                 330                 335
Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
            340                 345                 350
Phe Ser Tyr Ile Ala Gln Glu
        355
```

<210> 52
<211> 1920
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37k fiber

<221> CDS
<222> (13)...(1755)

<221> misc_feature
<222> 1867, 1875
<223> n = A,T,C or G

<400> 52

```
gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
              Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
               1               5                  10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt   99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
     15                  20                  25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg   147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30                  35                  40                  45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg   195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
                 50                  55                  60
```

```
ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac   243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
    65                  70                  75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc   291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
    80                  85                  90

aag tca aac ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca   339
Lys Ser Asn Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser
    95                 100                 105

gaa gcc cta act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac   387
Glu Ala Leu Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn
110                 115                 120                 125

aca ctc acc atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa   435
Thr Leu Thr Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys
                130                 135                 140

ctt agc att gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta   483
Leu Ser Ile Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu
            145                 150                 155

gcc ctg caa aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt   531
Ala Leu Gln Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu
        160                 165                 170

act atc act gcc tca ccc cct cta act act gcc act ggt agc ttg ggc   579
Thr Ile Thr Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly
    175                 180                 185

att gac ttg aaa gag ccc att tat aca caa aat gga aaa cta gga cta   627
Ile Asp Leu Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu
190                 195                 200                 205

aag tac ggg gct cct ttg cat gta aca gac gac cta aac act ttg acc   675
Lys Tyr Gly Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr
                210                 215                 220

gta gca act ggt cca ggt gtg act att aat aat act tcc ttg caa act   723
Val Ala Thr Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr
            225                 230                 235

aaa gtt act gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt   771
Lys Val Thr Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu
        240                 245                 250

aat gta gca gga gga cta agg att gat tct caa aac aga cgc ctt ata   819
Asn Val Ala Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile
    255                 260                 265

ctt gat gtt agt tat ccg ttt gat gct caa aac caa cta aat cta aga   867
Leu Asp Val Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg
270                 275                 280                 285

cta gga cag ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att   915
Leu Gly Gln Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile
                290                 295                 300
```

```
aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa   963
Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys
            305                 310                 315

aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct  1011
Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala
        320                 325                 330

aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct  1059
Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro
    335                 340                 345

aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta  1107
Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu
350                 355                 360                 365

gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt  1155
Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu
                370                 375                 380

agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat  1203
Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp
            385                 390                 395

aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att  1251
Lys Leu Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile
        400                 405                 410

gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga  1299
Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly
    415                 420                 425

agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac  1347
Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr
430                 435                 440                 445

cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att  1395
His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile
                450                 455                 460

aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt  1443
Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu
            465                 470                 475

gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca  1491
Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr
        480                 485                 490

gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca  1539
Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro
    495                 500                 505

aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act  1587
Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr
510                 515                 520                 525

ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc  1635
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr
                530                 535                 540

ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt  1683
```

```
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser
            545                 550                 555

tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc   1731
Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
        560                 565                 570

ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg  1785
Phe Ser Tyr Ile Ala Gln Glu  *
    575                 580

tttaaacccg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgtttgcc 1845
cctccccgt gccttccttg ancctggaan gtgccactcc cactgtcctt tcctaataaa 1905
atgaggaaat gcatc                                                  1920

<210> 53
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37k

<400> 53
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
        115                 120                 125
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                 170                 175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                 215                 220
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                 265                 270
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
```

```
    290                 295                 300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                 310                 315                 320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                325                 330                 335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340                 345                 350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355                 360                 365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370                 375                 380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                 390                 395                 400
Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp
                405                 410                 415
Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420                 425                 430
Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile
        435                 440                 445
Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu
    450                 455                 460
Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala
465                 470                 475                 480
Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu
                485                 490                 495
Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser
            500                 505                 510
Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu
        515                 520                 525
Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln
    530                 535                 540
Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys
545                 550                 555                 560
Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr
                565                 570                 575
Ile Ala Gln Glu
            580
```

<210> 54
<211> 1767
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s fiber

<221> CDS
<222> (13)...(1749)

<400> 54

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atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
              Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
               1               5                  10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt   99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
     15                  20                  25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg   147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
```

```
30                  35                  40                  45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg   195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
                50                  55                  60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc agc   243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser
            65                  70                  75

cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac   291
Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn
        80                  85                  90

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   339
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
    95                  100                 105

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   387
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
110                 115                 120                 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   435
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
                130                 135                 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   483
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
            145                 150                 155

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   531
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
        160                 165                 170

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   579
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
    175                 180                 185

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   627
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
190                 195                 200                 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   675
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
                210                 215                 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   723
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
            225                 230                 235

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca   771
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
        240                 245                 250

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt   819
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
    255                 260                 265

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag   867
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
270                 275                 280                 285
```

```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac   915
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
            290                 295                 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag   963
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
        305                 310                 315

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata  1011
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
    320                 325                 330

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca  1059
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
335                 340                 345

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat  1107
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
350                 355                 360                 365

tca aac att ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac  1155
Ser Asn Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp
            370                 375                 380

aat gat ggt gcc att aca gta gga aac aaa aat aat gat aag cta act  1203
Asn Asp Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
        385                 390                 395

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag  1251
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
    400                 405                 410

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata  1299
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
415                 420                 425

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata  1347
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
430                 435                 440                 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat  1395
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
            450                 455                 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt  1443
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
        465                 470                 475

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga  1491
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
    480                 485                 490

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc  1539
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
495                 500                 505

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa  1587
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
510                 515                 520                 525
```

```
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac   1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
                530                 535                 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc   1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
            545                 550                 555

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca   1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
        560                 565                 570

tac att gcc caa gaa taa agaagcggcc gcgttatg                      1767
Tyr Ile Ala Gln Glu  *
    575
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<210> 55
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s

<400> 55

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Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val
65                  70                  75                  80
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu
                85                  90                  95
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala
            100                 105                 110
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser
        115                 120                 125
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln
    130                 135                 140
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Thr Ser Gly
145                 150                 155                 160
Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro
                165                 170                 175
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro
            180                 185                 190
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu
        195                 200                 205
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly
    210                 215                 220
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu
225                 230                 235                 240
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu
                245                 250                 255
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro
            260                 265                 270
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu
```

```
        275                 280                 285
Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn Lys Gly Leu
    290                 295                 300
Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu Val Asn Leu
305                 310                 315                 320
Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile Ala Ile Asn
                325                 330                 335
Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro Asn Thr Asn
            340                 345                 350
Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp Ser Asn Ile
        355                 360                 365
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
    370                 375                 380
Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr Leu Trp Thr
385                 390                 395                 400
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
                405                 410                 415
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
            420                 425                 430
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
        435                 440                 445
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
    450                 455                 460
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
465                 470                 475                 480
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
                485                 490                 495
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
            500                 505                 510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
        515                 520                 525
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
    530                 535                 540
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
545                 550                 555                 560
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
                565                 570                 575
Gln Glu
```

<210> 56
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad37s/Ad5k fiber

<221> CDS
<222> (16)...(1116)

<221> misc_feature
<222> 1125
<223> n = A,T,C or G

<400> 56

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gtcgcaagat ccaag atg aag agg gcc cgg ccc agc gaa gat gac ttc aac  51
               Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
                1               5                  10
```

```
ccc gtc tac ccc tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc    99
Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu
        15                  20                  25

act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg   147
Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly
    30                  35                  40

gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat   195
Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp
45                  50                  55                  60

gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta   243
Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu
                65                  70                  75

act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt   291
Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu
            80                  85                  90

gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt   339
Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser
        95                  100                 105

tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg   387
Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala
    110                 115                 120

ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga   435
Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly
125                 130                 135                 140

ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att   483
Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile
                145                 150                 155

ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga   531
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
            160                 165                 170

tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc   579
Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr
        175                 180                 185

aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct   627
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
    190                 195                 200

aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca   675
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
205                 210                 215                 220

gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca   723
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
                225                 230                 235

gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta   771
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
            240                 245                 250

cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga   819
```

```
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
        255                 260                 265

gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct   867
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
    270                 275                 280

aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac   915
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
285                 290                 295                 300

att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca   963
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
                305                 310                 315

cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca  1011
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
            320                 325                 330

agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac  1059
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
        335                 340                 345

att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc  1107
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
    350                 355                 360

caa gaa taa agaagcggnc gctcga                                   1132
Gln Glu  *
365
```

<210> 57
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37s/Ad5k

<400> 57

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Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50                  55                  60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                85                  90                  95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
            100                 105                 110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115                 120                 125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130                 135                 140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                 150                 155                 160
```

```
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                165                 170                 175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Ala Pro
            180                 185                 190
Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu
        195                 200                 205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu
    210                 215                 220
Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala
225                 230                 235                 240
His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser
                245                 250                 255
Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu
            260                 265                 270
Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala
        275                 280                 285
Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln
    290                 295                 300
Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr
305                 310                 315                 320
Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser
                325                 330                 335
Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile
            340                 345                 350
Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
        355                 360                 365
```

<210> 58
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 third repeat

<400> 58

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Gly Ser Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp
 1               5                  10                  15
```

<210> 59
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad8 last repeat

<400> 59

```
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asp Asn
 1               5                  10
```

<210> 60
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad9 last repeat

<400> 60
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asn Asp
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 last repeat

<400> 61
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Glu Ala
1 5 10

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton region

<400> 62
His Ala Ile Arg Gly Asp Thr Phe
1 5

<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton amino acid replacement

<400> 63
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser
1 5 10 15

<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Fiber protein conserved sequence

<400> 64
Thr Trp Leu Thr
1

<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> HSP binding motif

<400> 65
Lys Lys Thr Lys
1

<210> 66
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad8 third repeat

<400> 66
Gly Lys Leu Thr Val Asn Thr Glu Pro Pro Leu His Leu Thr Asn Asn
1 5 10 15

<210> 67
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad9 third repeat

<400> 67
Gly Lys Leu Thr Val Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn
1 5 10 15

<210> 68
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 third repeat

<400> 68
Gly Asn Leu Thr Val Asn Thr Glu Pro Pro Leu Gln Leu Thr Asn Asn
1 5 10 15

<210> 69
<211> 3929
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector pCR2.1

<400> 69
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acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc 120
tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg 240
gtaccgagct cggatccact agtaacggcc gccagtgtgc tggaattcgg cttaagccga 300

attctgcaga tatccatcac actggcggcc gctcgagcat gcatctagag ggcccaattc 360
gccctatagt gagtcgtatt acaattcact ggccgtcgtt ttacaacgtc gtgactggga 420
aaaccctggc gttacccaac ttaatcgcct tgcagcacat ccccctttcg ccagctggcg 480
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ggctgcatac gcttgatccg gctacctgcc cattcgacca ccaagcgaaa catcgcatcg 1740
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tgcggccaac ttacttctga caacgatcgg aggaccgaag gagctaaccg ctttttgca 2580
caacatgggg gatcatgtaa ctcgccttga tcgttgggaa ccggagctga atgaagccat 2640
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